

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: January 9, 2003, 12:23:23 ; Search time 15 Seconds  
(without alignments)  
83.316 Million cell updates/sec

Title: US-09-632-429-4  
Perfect score: 89  
Sequence: 1 WEVLQWTWETCER 13

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR.73:.\*  
1: pir1:.\*  
2: pir2:.\*  
3: pir3:.\*  
4: pir4:.\*

pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	51	57.3	292	S70117	hypothetical prote
2	49	55.1	395	B96610	hypothetical prote
3	46	51.7	427	T41257	hypothetical prote
4	46	51.7	1080	T19048	probable Pro-X car
5	46	51.7	1121	T21303	hypothetical prote
6	46	51.7	1230	S47466	cellulose 1,4-beta
7	44	49.4	203	A53294	superoxide dismuta
8	43	48.3	536	T10000	cytochrome P450 (C
9	43	48.3	524	T09999	cytochrome P450 -
10	43	48.3	524	T09944	probable cytochrom
11	42	47.2	347	D69373	immunogenic protei
12	42	47.2	475	T45766	hypothetical prote
13	42	47.2	501	B85025	hypothetical prote
14	42	47.2	569	S75169	urease (EC 3.5.1.5
15	42	47.2	731	T09172	probable calcium-a
16	41.5	46.6	359	A22421	3-dehydroshikimate
17	41.5	46.6	519	S36808	methylmalonyl-CoA
18	41	46.1	242	E71621	ERCC1-like excisio
19	41	46.1	276	T47351	hypothetical prote
20	41	46.1	278	S48776	hypothetical prote
21	41	46.1	306	A75316	hypothetical prote
22	41	46.1	330	S08500	QUG protein - Eme
23	41	46.1	340	T31277	hypothetical prote
24	41	46.1	481	T10036	hypothetical prote
25	41	46.1	494	T16658	hypothetical prote
26	41	46.1	575	A96766	unknown protein F2
27	41	46.1	594	D71347	conserved hypothet
28	41	46.1	732	Ad0014	primosomal protein
29	41	46.1	856	G96814	hypothetical prote

30	41	46.1	951	2	T00260	hypothetical prote
31	41	46.1	1085	2	H82511	hypothetical prote
32	41	46.1	1711	2	T21432	hypothetical prote
33	40.5	45.5	1256	2	T47325	hypothetical prote
34	40.5	45.5	4861	2	S71752	giant protein p619
35	40	44.9	280	2	A70513	hypothetical prote
36	40	44.9	295	2	S46749	hypothetical prote
37	40	44.9	306	2	D87531	glycosyl transfera
38	40	44.9	415	2	T49840	hypothetical prote
39	40	44.9	416	2	G86232	cysteine proteinas
40	40	44.9	614	2	T19963	hypothetical prote
41	40	44.9	741	2	B49555	enhancer of split
42	40	44.9	855	2	T29775	hypothetical prote
43	39.5	44.4	348	2	JN0250	dehydroshikimate d
44	39.5	44.4	551	2	D75195	hypothetical prote
45	39	43.8	93	2	AC3330	hypothetical prote

ALIGNMENTS

RESULT 1

S70117

hypothetical protein YDR287w - yeast (Saccharomyces cerevisiae)

N:Alternate names: hypothetical protein p9819.7

C:Species: Saccharomyces cerevisiae

C>Date: 24-Aug-1996 #sequence\_revision 06-Sep-1996 #text\_change 19-Apr-2002

C:Accession: S70117

R:Fulton, L.

submitted to the EMBL Data Library, May 1996

A:Description: The sequence of S. cerevisiae cosmid 9819.

A:Reference number: S70114

A:Accession: S70117

A:Molecule type: DNA

A:Residues: 1-292 <FUI>

A:Cross-references: EMBL:U51031; NID:gl332635; PID:gl332637; GSPDB:GN00004; MIPS:YDR2

C:Genetics:

A:Gene: MIPS:YDR287w

A:Cross-references: SGD:S0002695

A:Map position: 4R

C:Superfamily: suppressor protein subB

Query Match 57.3%; Score 51; DB 2; Length 292;  
Best Local Similarity 54.5%; Pred. No. 3.3;  
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 WEVLQWTWETC 11

DB 223 WEGGCWAWDVC 233

RESULT 2

B96610

hypothetical protein T8L23.7 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse ear cress)

C>Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 31-Mar-2001

C:Accession: B96610

R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon

Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Creasy, T.H.; Dewar,

ansen, N.F.; Hughes, B.; Huizar, L.

Nature 400, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A86141; MUID:21016719; PMID:11130712

A:Accession: B96610

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-395 <STO>

A:Cross-references: GB:AE005173; NID:gl11055860; PIDN:AAG28328.1; GSPDB:GN00141

51.7%; Score 46; DB 2; Length 1080;

superoxide dismutase (EC 1.15.1.1) (Mn) - *Pseudomonas aeruginosa*  
 A53294  
 Species: *Pseudomonas aeruginosa*  
 C.Date: 03-Oct-1995 #sequence\_revision 03-Oct-1995 #text\_change 1  
 C.Accession: A53294; JG4981  
 R.Hasset, D.J.; Woodruff, W.A.; Wozniak, D.J.; Vasil, M.L.; Cohen  
 J. Bacteriol 175, 7658-7665, 1993

A:Title: Cloning and characterization of the *Pseudomonas aeruginosa* *sodA* and *sodB* genes  
 A:Reference number: A53294; MUID:94064560; PMID:8244935  
 A:Accession: A53294  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-203 <HAS>  
 A:Cross-references: GB:L25672  
 R:Polack, B.; Dacheux, D.; Delic-Attree, I.; Toussaint, B.; Vignais, P.M.  
 Biochem. Biophys. Res. Commun. 226, 555-560, 1996  
 A:Title: The *Pseudomonas aeruginosa* *fumC* and *sodA* genes belong to an iron-responsive operon  
 A:Reference number: JC4981; MUID:96400296; PMID:8806672  
 A:Accession: JC4981  
 A:Molecule type: DNA  
 A:Residues: 1-41, 'ALEGTPYAEQPVESLLRQLAGLPE', 66-203 <POL>  
 A:Cross-references: GB:U72494; NID:91628609; PIDN:AAB17391.1; PID:gl628613  
 A:Experimental source: strain CHA  
 C:Genetics:  
 A:Gene: *sodA*; Mn-SOD  
 C:Complex: homodimer  
 C:Function:  
 A:Description: catalyzes the dismutation of 2 molecules of peroxide radical to dioxygen  
 C:Superfamily: superoxide dismutase (Mn)  
 C:Keywords: homodimer; manganese; metalloprotein; oxidoreductase  
 F:27,81,164,168/Binding site: manganese (His, His, Asp, His) #status predicted

Query Match 49.4%; Score 44; DB 2; Length 203;  
 Best Local Similarity 46.2%; Pred. No. 24;  
 Matches 6; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 WEVLCWTWTCER 13  
 I:| | | | |  
 Db 53 WKVCCGNLVCRR 65

RESULT 8  
 T10000  
 C:Species: *Catharanthus roseus* (Madagascar periwinkle)  
 C:Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 16-Feb-2001  
 C:Accession: T10000  
 R:Mangold, U.; Eichel, J.; Batschauer, A.; Lanz, T.; Kaiser, T.; Spangenberg, G.; Werck-Plant Sci. 96, 129-136, 1994  
 A:Title: Gene and cDNA for plant cytochrome P450 proteins (CYP72 family) from *Catharanthus roseus*  
 A:Reference number: Z16915  
 A:Accession: T10000  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-516 <MAN>  
 A:Cross-references: EMBL:L19075; NID:g404689; PID:g404690  
 A:Experimental source: cv. cp3  
 C:Genetics:  
 A:Gene: CYP72C  
 C:Superfamily: unassigned cytochrome P450; cytochrome P450 homology  
 C:Keywords: heme; iron; metalloprotein  
 F:318-481/Domain: cytochrome P450 homology <P45>  
 F:459/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 48.3%; Score 43; DB 2; Length 516;  
 Best Local Similarity 53.8%; Pred. No. 75;  
 Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 WEVLCWTWTCER 13  
 I:| | | | |  
 Db 14 WRVLDNAWFTPKR 26

RESULT 9  
 T09999  
 C:Species: *Catharanthus roseus* (Madagascar periwinkle)  
 C:Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 16-Feb-2001  
 C:Accession: T09999

R:Mangold, U.; Eichel, J.; Batschauer, A.; Lanz, T.; Kaiser, T.; Spangenberg, G.; Werck-Plant Sci. 96, 129-136, 1994  
 A:Title: Gene and cDNA for plant cytochrome P450 proteins (CYP72 family) from *Catharanthus roseus*  
 A:Reference number: Z16915  
 A:Accession: T09999  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-524 <MAN>  
 A:Cross-references: EMBL:L19074; NID:g404687; PID:g404688  
 A:Experimental source: cv. cp3  
 C:Genetics:  
 A:Gene: CYP72B  
 A:Introns: 96/1; 170/3; 252/2; 381/3  
 C:Superfamily: human cytochrome P450 CYP4B1; cytochrome P450 homology  
 C:Keywords: heme; iron; metalloprotein  
 F:329-492/Domain: cytochrome P450 homology <P45>  
 F:470/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 48.3%; Score 43; DB 2; Length 524;  
 Best Local Similarity 53.8%; Pred. No. 76;  
 Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 WEVLCWTWTCER 13  
 I:| | | | |  
 Db 25 WRVLDNAWFTPKR 37

RESULT 10  
 T09944  
 probable cytochrome P450 protein - Madagascar periwinkle  
 N:Alternate names: CYP72 protein  
 C:Species: *Catharanthus roseus* (Madagascar periwinkle)  
 C:Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 16-Feb-2001  
 C:Accession: T09944  
 R:Vetter, H.P.; Mangold, U.; Schroeder, G.; Marner, F.J.; Werck-Reichhart, D.; Schroeder Plant Physiol. 100, 998-1007, 1992  
 A:Title: Molecular analysis and heterologous expression of an inducible cytochrome P-plant  
 A:Reference number: Z16902  
 A:Accession: T09944  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-524 <VET>  
 A:Cross-references: EMBL:L10081; NID:gl67483; PID:gl67484  
 C:Genetics:  
 A:Gene: CYP72  
 C:Superfamily: human cytochrome P450 CYP4B1; cytochrome P450 homology  
 C:Keywords: heme; iron; metalloprotein  
 F:329-492/Domain: cytochrome P450 homology <P45>  
 F:470/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 48.3%; Score 43; DB 2; Length 524;  
 Best Local Similarity 53.8%; Pred. No. 76;  
 Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 WEVLCWTWTCER 13  
 I:| | | | |  
 Db 25 WRVLDNAWFTPKR 37

RESULT 11  
 D69373  
 immunogenic protein (bcsp31-3) homolog - *Archaeoglobus fulgidus*  
 C:Species: *Archaeoglobus fulgidus*  
 C:Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 17-Mar-2000  
 C:Accession: D69373  
 R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dod-; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.; Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.  
 Nature 390, 364-370, 1997  
 A:Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, Smith, H.O.; Woese, C.R.; Venter, J.C.  
 A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing arch  
 A:Reference number: A69250; MUID:98049343; PMID:9389475

A:Accession: D69373  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-347 <KLE>  
A:Cross-references: GB:AE001036; GB:AE000782; NID:g2689359; PIDN:AAB90255.1; PID:g264961  
C:Superfamily: immunogenic protein BCSP31

Query Match 47.2%; Score 42; DB 2; Length 347;  
Best Local Similarity 54.5%; Pred. No. 74;  
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 EVLCWTWETCE 12  
|||:|:|  
Db 35 EVKPSWATCD 45

RESULT 12  
T45766  
hypothetical protein F24M12.390 - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 04-Feb-2000 #sequence\_revision 04-Feb-2000 #text\_change 20-Jun-2000  
C:Accession: T45766  
R:Vitale, D.; Liguori, R.; Flores, M.; Argirou, A.; De Simone, V.; Mewes, H.W.; Lemcke, submitted to the Protein Sequence Database, December 1999  
A:Reference number: Z23012  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-475 <VIT>  
A:Cross-references: EMBL:AL132980  
A:Experimental source: cultivar Columbia; BAC clone F24M12  
C:Genetics:  
A:Map position: 3  
A:Introns: 100/2; 147/3; 225/2; 302/2; 319/2; 356/3; 375/3; 399/1  
A:Note: F24M12.390  
C:Superfamily: Arabidopsis thaliana hypothetical protein F24M12.380

Query Match 47.2%; Score 42; DB 2; Length 475;  
Best Local Similarity 60.0%; Pred. No. 97;  
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 VLQWTWETCE 12  
|:|:|:|  
Db 15 VVCGWGERCE 24

RESULT 13  
E85025  
hypothetical protein AT4g01990 [imported] - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 16-Feb-2001  
C:Accession: E85025  
R:anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring Nature 402, 769-777, 1999  
A:title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.  
A:Reference number: A85001; MUID:20083488; PMID:10617198  
A:Accession: E85025  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-501 <STO>  
A:Cross-references: GB:NC\_001268; NID:g7268583; PIDN:CAB80692.1; GSPDB:GN00140  
C:Genetics:  
A:Gene: AT4g01990  
A:Map position: 4

Query Match 47.2%; Score 42; DB 2; Length 501;  
Best Local Similarity 55.6%; Pred. No. 1e+02;  
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 WEVLCWTWE 9  
|||:|:|  
Db 341 WESTCWTYD 349

RESULT 14  
S75169  
urease (EC 3.5.1.5) alpha chain - Synechocystis sp. (strain PCC 6803)  
N:Alternate names: protein sll1750  
C:Species: Synechocystis sp.  
A:Variety: PCC 6803  
C:Date: 25-Apr-1997 #sequence\_revision 25-Apr-1997 #text\_change 20-Jun-2000  
C:Accession: S75169  
R:Kaneke, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, O., K.; Okumura, S.; Shimpou, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yas DNA Res. 3, 109-136, 1996  
A:title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis s.  
A:Reference number: S74322; MUID:97061201; PMID:8905231  
A:Accession: S75169  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-569 <KAN>  
A:Cross-references: EMBL:D90903; GB:AB001339; NID:gl652127; PIDN:BAAL7083.1; PID:g165  
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996  
C:Genetics:  
A:Gene: ureC  
C:Superfamily: urease 62K chain; urease 62K chain homology  
C:Keywords: hydrolase; metalloprotein; nickel  
F:5-552/Domain: urease 62K chain homology <U62>  
F:136,138,219,362/Binding site: nickel 2 (His, His, Lys, Asp) #status predicted

Query Match 47.2%; Score 42; DB 2; Length 569;  
Best Local Similarity 50.0%; Pred. No. 1.1e+02;  
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 EVLCWTWETCER 13  
||:|:|:|  
Db 371 EVICRTWQTAHK 382

RESULT 15  
T09172  
probable calcium-activated potassium channel KCNN3 - human  
C:Species: Homo sapiens (man)  
C:Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 11-May-2000  
C:Accession: T09172  
R:Chandy, K.G.; Fantino, E.; Wittekindt, O.; Kalman, K.; Tong, L.L.; Ho, T.H.; Gutman Mol. Psychiatry 3, 32-37, 1998  
A:title: Isolation of a novel potassium channel gene hSKCa3 containing a polymorphic  
A:Reference number: Z16601; MUID:98150774; PMID:9491810  
A:Accession: T09172  
A:Status: translated from GB/EMBL/DDBJ  
A:Molecule type: mRNA  
A:Residues: 1-731 <CHA>  
A:Cross-references: EMBL:AF031815; NID:g3309530; PID:g3309531  
C:Genetics:  
A:Gene: KCNN3  
C:Keywords: potassium channel; schizophrenia

Query Match 47.2%; Score 42; DB 2; Length 731;  
Best Local Similarity 46.2%; Pred. No. 1.4e+02;  
Matches 6; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 WEVLCWTWETCER 13  
|:|:|:|  
Db 471 WIIAAWTVRACER 483

Search completed: January 9, 2003, 12:25:09  
Job time : 16 secs